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PCT

```
         RAW SEQUENCE LISTING              DATE: 06/22/2005
         PATENT APPLICATION:  US/10/538,471    TIME: 10:19:58

         Input Set : A:\PTO.RJ.txt
         Output Set: N:\CRF4\06222005\J538471.raw


     3 <110> APPLICANT: Balakireva, Larissa
     5 <120> TITLE OF INVENTION: MOLECULES INHIBITING HEPATITIS C VIRUS PROTEIN SYNTHESIS AND
METHOD FOR
     6       SCREENING SAME
     8 <130> FILE REFERENCE: 1759.200
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/538,471
C--> 11 <141> CURRENT FILING DATE: 2005-06-03
    11 <150> PRIOR APPLICATION NUMBER: PCT/FR03/03675
    12 <151> PRIOR FILING DATE: 2003-12-11
    14 <150> PRIOR APPLICATION NUMBER: FR0215718
    15 <151> PRIOR FILING DATE: 2002-12-12
    17 <160> NUMBER OF SEQ ID NOS: 16
    19 <170> SOFTWARE: PatentIn version 3.1
    21 <210> SEQ ID NO: 1
    22 <211> LENGTH: 326
    23 <212> TYPE: DNA
    24 <213> ORGANISM: Artificial Sequence
W--> 26 <220> FEATURE: <221> HCV
    27 <222> LOCATION: 40..372
    28 <223> OTHER INFORMATION: corresponds to IRES sequence of HCV
    30 <400> SEQUENCE: 1
    32 ctcccctgtg aagaactact gtcttcacgc agaaagcgtc tagccatggc gttagtatga    60
    34 gtgtcgtgca gcctccagga ccccccctcc cgggagagcc atagtggtct gcggaaccgg   120
    36 tgagtacacc ggaattgcca ggatgaccgg gtcctttctt ggatcaaccc gctcaatgcc   180
    38 tggagatttg ggcgtgcccc cgcgagactg ctagccgagt agtgttgggt cgcgaaaggc   240
    40 cttgtggtac tgcctgatag ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca   300
    42 tcatgagcac aaatcctaaa gaaaaa                                          326
    45 <210> SEQ ID NO: 2
    46 <211> LENGTH: 80
    47 <212> TYPE: DNA
    48 <213> ORGANISM: Artificial Sequence
W--> 50 <220> FEATURE: <221> HCV
    51 <222> LOCATION: 40..119
    52 <223> OTHER INFORMATION: corresponds to a portion (region II) of HCV IRES sequence
    54 <400> SEQUENCE: 2
    56 ctcccctgtg aggaactact gtcttcacgc agaaagcgtc tagccatggc gttagtatga    60
    58 gtgttgtgca gcctccagga                                                 80
    61 <210> SEQ ID NO: 3
    62 <211> LENGTH: 37
    63 <212> TYPE: DNA
    64 <213> ORGANISM: Artificial Sequence
W--> 66 <220> FEATURE: <221> HCV
    67 <222> LOCATION: 56..92
    68 <223> OTHER INFORMATION: corresponds to a portion (consensus sequence) of HCV IRES
```

Does Not Comply Corrected Diskette Needed

(pg 1, 3-6)

- moved <221> response to next line?

same

same

sequence

RAW SEQUENCE LISTING   DATE: 06/22/2005
PATENT APPLICATION: US/10/538,471   TIME: 10:19:58

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06222005\J538471.raw**

```
 70  <400> SEQUENCE: 3
 72  tactgtcttc acgcagaaag cgtctagcca tggcgtt                          37
 75  <210> SEQ ID NO: 4
 76  <211> LENGTH: 814
 77  <212> TYPE: PRT
 78  <213> ORGANISM: Artificial Sequence        same
W--> 80 <220> FEATURE: <221> p116
 81  <222> LOCATION: 1..814
 82  <223> OTHER INFORMATION: corresponds to p116 subunit of eIF3
 84  <400> SEQUENCE: 4
 86  Met Gln Asp Ala Glu Asn Val Ala Val Pro Glu Ala Ala Glu Glu Arg
 87  1               5                  10                  15
 90  Ala Glu Pro Gly Gln Gln Gln Pro Ala Ala Glu Pro Pro Pro Ala Glu
 91              20                  25                  30
 94  Gly Leu Leu Arg Pro Ala Gly Pro Gly Ala Pro Glu Ala Ala Gly Thr
 95              35                  40                  45
 98  Glu Ala Ser Ser Glu Glu Val Gly Ile Ala Glu Ala Gly Pro Glu Pro
 99       50                  55                  60
102  Glu Val Arg Thr Glu Pro Ala Ala Glu Ala Glu Ala Ala Ser Gly Pro
103  65                  70                  75                  80
106  Ser Glu Ser Pro Ser Pro Pro Ala Ala Glu Glu Leu Pro Gly Ser His
107              85                  90                  95
110  Ala Glu Pro Pro Val Pro Ala Gln Gly Glu Ala Pro Gly Glu Gln Ala
111              100                 105                 110
114  Arg Asp Glu Arg Ser Asp Ser Arg Ala Gln Ala Val Ser Glu Asp Ala
115          115                 120                 125
118  Gly Gly Asn Glu Gly Arg Ala Ala Glu Ala Glu Pro Arg Ala Leu Glu
119      130                 135                 140
122  Asn Gly Asp Ala Asp Glu Pro Ser Phe Ser Asp Pro Glu Asp Phe Val
123  145                 150                 155                 160
126  Asp Asp Val Ser Glu Glu Glu Leu Leu Gly Asp Val Leu Lys Asp Arg
127              165                 170                 175
130  Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val Asp Asn Val
131          180                 185                 190
134  Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn Val Ile His
135          195                 200                 205
138  Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe Tyr Pro Glu
139      210                 215                 220
142  Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr Ala Ser Pro
143  225                 230                 235                 240
146  Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr Lys Leu Asp
147              245                 250                 255
150  Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe Asp Lys Tyr
151          260                 265                 270
154  Met Thr Ile Ser Asp Glu Trp Asp Ile Pro Glu Lys Gln Pro Phe Lys
155          275                 280                 285
158  Asp Leu Gly Asn Leu Arg Tyr Trp Leu Glu Glu Ala Glu Cys Arg Asp
159      290                 295                 300
162  Gln Tyr Ser Val Ile Phe Glu Ser Gly Asp Arg Thr Ser Ile Phe Trp
```

```
163 305                   310                 315                 320
166 Asn Asp Val Lys Asp Pro Val Ser Ile Glu Glu Arg Ala Arg Trp Thr
167             325                 330                 335
170 Glu Thr Tyr Val Arg Trp Ser Pro Lys Gly Thr Tyr Leu Ala Thr Phe
171             340                 345                 350
174 His Gln Arg Gly Ile Ala Leu Trp Gly Gly Glu Lys Phe Lys Gln Ile
175             355                 360                 365
178 Gln Arg Phe Ser His Gln Gly Val Gln Leu Ile Asp Phe Ser Pro Cys
179       370                 375                 380
182 Glu Arg Tyr Leu Val Thr Phe Ser Pro Leu Met Asp Thr Gln Asp Asp
183 385                 390                 395                 400
186 Pro Gln Ala Ile Ile Ile Trp Asp Ile Leu Thr Gly His Lys Lys Arg
187                 405                 410                 415
190 Gly Phe His Cys Glu Ser Ser Ala His Trp Pro Ile Phe Lys Trp Ser
191             420                 425                 430
194 His Asp Gly Lys Phe Phe Ala Arg Met Thr Leu Asp Thr Leu Ser Ile
195             435                 440                 445
198 Tyr Glu Thr Pro Ser Met Gly Leu Leu Asp Lys Lys Ser Leu Lys Ile
199       450                 455                 460
202 Ser Gly Ile Lys Asp Phe Ser Trp Ser Pro Gly Gly Asn Ile Ile Ala
203 465                 470                 475                 480
206 Phe Trp Val Pro Glu Asp Lys Asp Ile Pro Ala Arg Val Thr Leu Met
207             485                 490                 495
210 Gln Leu Pro Thr Arg Gln Glu Ile Arg Val Arg Asn Leu Phe Asn Val
211             500                 505                 510
214 Val Asp Cys Lys Leu His Trp Gln Lys Asn Gly Asp Tyr Leu Cys Val
215       515                 520                 525
218 Lys Val Asp Arg Thr Pro Lys Gly Thr Gln Gly Val Val Thr Asn Phe
219       530                 535                 540
222 Glu Ile Phe Arg Met Arg Glu Lys Gln Val Pro Val Asp Val Val Glu
223 545                 550                 555                 560
226 Met Lys Glu Thr Ile Ile Ala Phe Ala Trp Glu Pro Asn Gly Ser Lys
227             565                 570                 575
230 Phe Ala Val Leu His Gly Glu Ala Pro Arg Ile Ser Val Ser Phe Tyr
231             580                 585                 590
234 His Val Lys Asn Asn Gly Lys Ile Glu Leu Ile Lys Met Phe Asp Lys
235       595                 600                 605
238 Gln Gln Ala Asn Thr Ile Phe Trp Ser Pro Gln Gly Gln Phe Val Val
239       610                 615                 620
242 Leu Ala Gly Leu Arg Ser Met Asn Gly Ala Leu Ala Phe Val Asp Thr
243 625                 630                 635                 640
246 Ser Asp Cys Thr Val Met Asn Ile Ala Glu His Tyr Met Ala Ser Asp
247             645                 650                 655
250 Val Glu Trp Asp Pro Thr Gly Arg Tyr Val Val Thr Ser Val Ser Trp
251             660                 665                 670
254 Trp Ser His Lys Val Asp Asn Ala Tyr Trp Leu Trp Thr Phe Gln Gly
255       675                 680                 685
258 Arg Leu Leu Gln Lys Asn Asn Lys Asp Arg Phe Cys Gln Leu Leu Trp
259       690                 695                 700
```

```
262 Arg Pro Arg Pro Pro Thr Leu Leu Ser Gln Glu Gln Ile Lys Gln Ile
263 705             710             715                 720
266 Lys Lys Asp Leu Lys Lys Tyr Ser Lys Ile Phe Glu Gln Lys Asp Arg
267             725             730                 735
270 Leu Ser Gln Ser Lys Ala Ser Lys Glu Leu Val Glu Arg Arg Arg Thr
271             740             745             750
274 Met Met Glu Asp Phe Arg Lys Tyr Arg Lys Met Ala Gln Glu Leu Tyr
275         755             760             765
278 Met Glu Gln Lys Asn Glu Arg Leu Glu Leu Arg Gly Gly Val Asp Thr
279     770             775             780
282 Asp Glu Leu Asp Ser Asn Val Asp Asp Trp Glu Glu Glu Thr Ile Glu
283 785             790             795                 800
286 Phe Phe Val Thr Glu Glu Ile Ile Pro Leu Gly Asn Gln Glu
287             805             810
290 <210> SEQ ID NO: 5
291 <211> LENGTH: 106
292 <212> TYPE: PRT
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE: <221> p116
296 <222> LOCATION: 175..279
297 <223> OTHER INFORMATION: corresponds to a portion (RRM) of eIF3 p116 subunit
299 <400> SEQUENCE: 5
301 Met Asp Arg Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val
302 1             5             10                 15
305 Asp Asn Val Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn
306             20             25             30
309 Val Ile His Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe
310         35             40             45
313 Tyr Pro Glu Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr
314     50             55             60
317 Ala Ser Pro Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr
318 65             70             75                 80
321 Lys Leu Asp Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe
322             85             90             95
325 Asp Lys Tyr Met Thr Ile Ser Asp Glu Trp
326             100             105
329 <210> SEQ ID NO: 6
330 <211> LENGTH: 33
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE: <221> primer_bind
335 <222> LOCATION: 1..33
336 <223> OTHER INFORMATION: HCV RRM 5' primer (RRMfwd)
338 <400> SEQUENCE: 6
340 catatggatc ggccccagga agcagatgga atc                         33
343 <210> SEQ ID NO: 7
344 <211> LENGTH: 33
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
```

W--> (annotation near line 295) same
W--> (annotation near line 334) same

RAW SEQUENCE LISTING   DATE: 06/22/2005
PATENT APPLICATION: US/10/538,471   TIME: 10:19:58

                    Input Set : A:\PTO.RJ.txt
                    Output Set: N:\CRF4\06222005\J538471.raw

W--> 348 <220> FEATURE: <221> primer_bind   ← Same
     349 <222> LOCATION: 1..33
     350 <223> OTHER INFORMATION: HCV RRM 3' primer (RRMrev)
     352 <400> SEQUENCE: 7
     354 gtgctcgagc cactcgtcac tgatcgtcat ata   33
     357 <210> SEQ ID NO: 8
     358 <211> LENGTH: 29
     359 <212> TYPE: DNA
     360 <213> ORGANISM: Artificial Sequence   ← Same
W--> 362 <220> FEATURE: <221> primer_bind.   ← Same
     363 <222> LOCATION: 1..29
     364 <223> OTHER INFORMATION: HCV IRES 5' primer (IRESfwd)
     366 <400> SEQUENCE: 8
     368 accgctagcc tcccctgtga ggaactact   29
     371 <210> SEQ ID NO: 9
     372 <211> LENGTH: 46
     373 <212> TYPE: DNA
     374 <213> ORGANISM: Artificial Sequence   ← Same
W--> 376 <220> FEATURE: <221> primer_bind   ← Same
     377 <222> LOCATION: 1..46
     378 <223> OTHER INFORMATION: HCV IRES 3' primer (IRESrev)
     380 <400> SEQUENCE: 9
     382 gaaagctttt ttctttgagg tttaggattt gtgctcatga tgcacg   46
     385 <210> SEQ ID NO: 10
     386 <211> LENGTH: 95
     387 <212> TYPE: DNA
     388 <213> ORGANISM: Artificial Sequence   ← Same
W--> 390 <220> FEATURE: <221> primer_bind   ← Same
     391 <222> LOCATION: 1..95
     392 <223> OTHER INFORMATION: primer IIIabcfwd which corresponds to T7 polymerase promoter
+ 139-215 of
     393   HCV (regions IIIa-IIIb)
     395 <400> SEQUENCE: 10
     397 taatacgact cactataggg tagtggtctg cggaaccggt gagtacaccg gaattgccag   60
     399 gacgaccggg tcctttcttg gataaacccg ctcaa   95
     402 <210> SEQ ID NO: 11
     403 <211> LENGTH: 60
     404 <212> TYPE: DNA
     405 <213> ORGANISM: Artificial Sequence   ← Same
W--> 407 <220> FEATURE: <221> primer_bind   ← Same
     408 <222> LOCATION: 1..60
     409 <223> OTHER INFORMATION: primer IIIabcrev which corresponds to 193-252 of HCV
(regions IIIb-IIIc)
     413 <400> SEQUENCE: 11
     415 tagcagtctc gcgggggcac gcccaaatct ccaggcattg agcgggttga tccaagaaag   60
     418 <210> SEQ ID NO: 12
     419 <211> LENGTH: 20
     420 <212> TYPE: DNA
     421 <213> ORGANISM: Artificial Sequence   ← Same
W--> 423 <220> FEATURE: <221> primer_bind   ← Same
     424 <222> LOCATION: 1..20

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/22/2005
PATENT APPLICATION: US/10/538,471   TIME: 10:19:59

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06222005\J538471.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:10; Line(s) 392

$L-72.$

VERIFICATION SUMMARY   DATE: 06/22/2005
PATENT APPLICATION: **US/10/538,471**   TIME: 10:19:59

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06222005\J538471.raw**

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:50 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:66 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:80 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:295 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:334 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:348 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:362 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:376 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:390 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:407 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:423 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:437 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:453 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:467 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:481 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
```